```
   1  TCTGGGAAGG AGGCCAGGAG TGGGGCAGGT CAACTGACTG GGAGCAGGGG
  51  ATCTGGGTTC CAAGAAGGAG TTGTGTTTGA GGTGGGGTCT GGGTCCTCGT
 101  GGAAGTCAGG ACTCCCAGGC AGAAAAGAGG CAGGCTGCAG GGAAGTAAGG
 151  AGGAGGCATG GCACCTTCTC ATCGGGCATC ACAGGTGGGG TTTTGCCCCA
 201  CCCCTGAACG CCCTCTGTGG CGCCTTCCAC CCACCTGTAG GCCCAGAAGG
 251  ATGTCGGTCT GCTACCGTCC CCCAGGGAAC GAGACACTGC TGAGCTGGAA
 301  GACTTCGCGG GCCACAGGCA CAGCCTTCCT GCTGCTGGCG GCGCTGCTGG
 351  GGCTGCCTGG CAACGGTTTC GTGGTGTGGA GCTTGGCGGG CTGGCGGCTT
 401  GCACGGGGGC GACCGCTGGC GGCAACGCTT GTGTTGCACC TGGCGCTGGC
 451  CGACGGCGCG GTGCTGCTGC TCACGCCGTT CTTTGTGGCC TTCCTGACCC
 501  GGCAGGCTTG GCCGCTGGGC CAGGCGGGCT GCAAGGCGGT GTACTACGTG
 551  TGCGCGCTCA GCATGTACGC CAGCGTGCTG CTCACCGGCC TGCTCAGCCT
 601  GCAGCGCTGC TTCGCAGTCA CCCGCCCCTT CCTGGCGCTT CGGCTGCGCA
 651  GCCCGGCCCT GGCCCGCCGC CTGCTGCTGG CGGTCTGGCT GGCCGCCCTG
 701  TTGCTCGCCG TCCCGGCCGC CGTCTACCGC CACCTGTGGA GGGACCGCGT
 751  ATGCCAGCTG TGCCACCCGT CGCCGGTCCA CGCCGCCGCC CACCTGAGCC
 801  TGGAGACTCT GACCGCTTTC GTGCTTCCTT TCGGGCTGAT GCTCGGCTGC
 851  TACAGCGTGA CGCTGGCACG GCTGCGGGGC GCCCGCTGGG GCTCCGGGCG
 901  GCACGGGGCG CGGGTGGGCC GGCTGGTGAG CGCCATCGTG CTTGCCTTCG
 951  GCTTGCTCTG GGCCCCCTAC CACGCAGTCA ACCTTCTGCA GGCGGTCGCA
1001  GCGCTGGCTC CACCGGAAGG GGCCTTGGCG AAGCTGGGCG GAGCCGGCCA
1051  GGCGGCGCGA GCGGGAACTA CGGCCTTGGC CTTCTTCAGT TCTAGCGTCA
1101  ACCCGGTGCT CTACGTCTTC ACCGCTGGAG ATCTGCTGCC CCGGGCAGGT
1151  CCCCGTTTCC TCACGCGGCT CTTCGAAGGC TCTGGGGAGG CCCGAGGGGG
1201  CGGCCGCTCT AGGGAAGGGA CCATGGAGCT CCGAACTACC CCTCAGCTGA
1251  AAGTGGTGGG GCAGGGCCGC GGCAATGGAG ACCCGGGGGG TGGGATGGAG
1301  AAGGACGGTC CGGAATGGGA CCTTTGACAG CAGACCCTAC AACCTGCTGC
1351  CCTTCCCTGT CCCTTTCCAC CCCCCACCCA CCCTCCAGAG GTCAGTGTTC
1401  TGGGACATTT GGGGACCCTT CTTTGACTAG AGTTTGGATC TGGCTGGGTA
1451  GGATTAGTAT ACACTTGGGG CAGGCCCAGG CTCCTCCAAA CTGAGGGATT
1501  ATGAGGGTGG TGATGGTCCC TGTTAAGGAC TATTGTGTGC TTGCAAGTTG
```

FIG. 1

```
  1  MAPSHRASQV GFCPTPERPL WRLPPTCRPR RMSVCYRPPG NETLLSWKTS
 51  RATGTAFLLL AALLGLPGNG FVVWSLAGWR LARGRPLAAT LVLHLALADG
101  AVLLLTPFFV AFLTRQAWPL GQAGCKAVYY VCALSMYASV LLTGLLSLQR
151  CFAVTRPFLA LRLRSPALAR RLLLAVWLAA LLLAVPAAVY RHLWRDRVCQ
201  LCHPSPVHAA AHLSLETLTA FVLPFGLMLG CYSVTLARLR GARWGSGRHG
251  ARVGRLVSAI VLAFGLLWAP YHAVNLLQAV AALAPPEGAL AKLGGAGQAA
301  RAGTTALAFF SSSVNPVLYV FTAGDLLPRA GPRFLTRLFE GSGEARGGGR
351  SREGTMELRT TPQLKVVGQG RGNGDPGGGM EKDGPEWDL
```

FIG.2

```
        10                  30                  50
CTGGGAAGGAGGCCAGGAGTGGGGCAGGTCAACTGACTGGGAGCAGGGGATCTGGGTTCC

        70                  90                  110
AAGAAGGAGTTGTGTTTGAGGTGGGGTCTGGGTCCTCGTGGAAGTCAGGACTCCCAGGCA

       130                 150                 170
GAAAAGAGGCAGGCTGCAGGGAAGTAAGGAGGAGGCATGGCACCTTCTCATCGGGCATCA
                                        MetAlaProSerHisArgAlaSer

       190                 210                 230
CAGGTGGGGTTTTGCCCCACCCCTGAACGCCCTCTGTGGCGCCTTCCACCCACCTGTAGG
GlnValGlyPheCysProThrProGluArgProLeuTrpArgLeuProProThrCysArg

       250                 270                 290
CCCAGAAGGATGTCGGTCTGCTACCGTCCCCCAGGGAACGAGACACTGCTGAGCTGGAAG
ProArgArgMetSerValCysTyrArgProProGlyAsnGluThrLeuLeuSerTrpLys

       310                 330                 350
ACTTCGCGGGCCACAGGCACAGCCTTCCTGCTGCTGGCGGCGCTGCTGGGGCTGCCTGGC
ThrSerArgAlaThrGlyThrAlaPheLeuLeuLeuAlaAlaLeuLeuGlyLeuProGly

       370                 390                 410
AACGGTTTCGTGGTGTGGAGCTTGGCGGGCTGGCGGCTTGCACGGGGGCGACCGCTGGCG
AsnGlyPheValValTrpSerLeuAlaGlyTrpArgLeuAlaArgGlyArgProLeuAla

       430                 450                 470
GCAACGCTTGTGTTGCACCTGGCGCTGGCCGACGGCGCGGTGCTGCTGCTCACGCCGTTC
AlaThrLeuValLeuHisLeuAlaLeuAlaAspGlyAlaValLeuLeuLeuThrProPhe

       490                 510                 530
TTTGTGGCCTTCCTGACCCGGCAGGCTTGGCCGCTGGGCCAGGCGGGCTGCAAGGCGGTG
PheValAlaPheLeuThrArgGlnAlaTrpProLeuGlyGlnAlaGlyCysLysAlaVal

       550                 570                 590
TACTACGTGTGCGCGCTCAGCATGTACGCCAGCGTGCTGCTCACCGGCCTGCTCAGCCTG
TyrTyrValCysAlaLeuSerMetTyrAlaSerValLeuLeuThrGlyLeuLeuSerLeu

       610                 630                 650
CAGCGCTGCTTCGCAGTCACCCGCCCCTTCCTGGCGCTTCGGCTGCGCAGCCCGGCCCTG
GlnArgCysPheAlaValThrArgProPheLeuAlaLeuArgLeuArgSerProAlaLeu

       670                 690                 710
GCCCGCCGCCTGCTGCTGGCGGTCTGGCTGGCCGCCCTGTTGCTCGCCGTCCCGGCCGCC
AlaArgArgLeuLeuLeuAlaValTrpLeuAlaAlaLeuLeuLeuAlaValProAlaAla

       730                 750                 770
GTCTACCGCCACCTGTGGAGGGACCGCGTATGCCAGCTGTGCCACCCGTCGCCGGTCCAC
ValTyrArgHisLeuTrpArgAspArgValCysGlnLeuCysHisProSerProValHis
```

FIG 3A

```
      790                   810                   830
GCCGCCGCCCACCTGAGCCTGGAGACTCTGACCGCTTTCGTGCTTCCTTTCGGGCTGATG
AlaAlaAlaHisLeuSerLeuGluThrLeuThrAlaPheValLeuProPheGlyLeuMet

      850                   870                   890
CTCGGCTGCTACAGCGTGACGCTGGCACGGCTGCGGGGCGCCCGCTGGGGCTCCGGGCGG
LeuGlyCysTyrSerValThrLeuAlaArgLeuArgGlyAlaArgTrpGlySerGlyArg

      910                   930                   950
CACGGGGCGCGGGTGGGCCGGCTGGTGAGCGCCATCGTGCTTGCCTTCGGCTTGCTCTGG
HisGlyAlaArgValGlyArgLeuValSerAlaIleValLeuAlaPheGlyLeuLeuTrp

      970                   990                  1010
GCCCCCTACCACGCAGTCAACCTTCTGCAGGCGGTCGCAGCGCTGGCTCCACCGGAAGGG
AlaProTyrHisAlaValAsnLeuLeuGlnAlaValAlaAlaLeuAlaProProGluGly

     1030                  1050                  1070
GCCTTGGCGAAGCTGGGCGGAGCCGGCCAGGCGGCGCGAGCGGGAACTACGGCCTTGGCC
AlaLeuAlaLysLeuGlyGlyAlaGlyGlnAlaAlaArgAlaGlyThrThrAlaLeuAla

     1090                  1110                  1130
TTCTTCAGTTCTAGCGTCAACCCGGTGCTCTACGTCTTCACCGCTGGAGATCTGCTGCCC
PhePheSerSerSerValAsnProValLeuTyrValPheThrAlaGlyAspLeuLeuPro

     1150                  1170                  1190
CGGGCAGGTCCCCGTTTCCTCACGCGGCTCTTCGAAGGCTCTGGGGAGGCCCGAGGGGGC
ArgAlaGlyProArgPheLeuThrArgLeuPheGluGlySerGlyGluAlaArgGlyGly

     1210                  1230                  1250
GGCCGCTCTAGGGAAGGGACCATGGAGCTCCGAACTACCCCTCAGCTGAAAGTGGTGGGG
GlyArgSerArgGluGlyThrMetGluLeuArgThrThrProGlnLeuLysValValGly

     1270                  1290                  1310
CAGGGCCGCGGCAATGGAGACCCGGGGGGTGGGATGGAGAAGGACGGTCCGGAATGGGAC
GlnGlyArgGlyAsnGlyAspProGlyGlyGlyMetGluLysAspGlyProGluTrpAsp

     1330                  1350                  1370
CTTTGACAGCAGACCCTACAACCTGCTGCCCTTCCCTGTCCCTTTCCACCCCCACCCAC
Leu

     1390                  1410                  1430
CCTCCAGAGGTCAGTGTTCTGGGACATTTGGGGACCCTTCTTTGACTAGAGTTTGGATCT

     1510                  1530                  1550
TGAGGGTGGTGATGGTCCCTGTTAAGGACTATTGTGTGCTTGCAAGTTG
```

FIG.3B

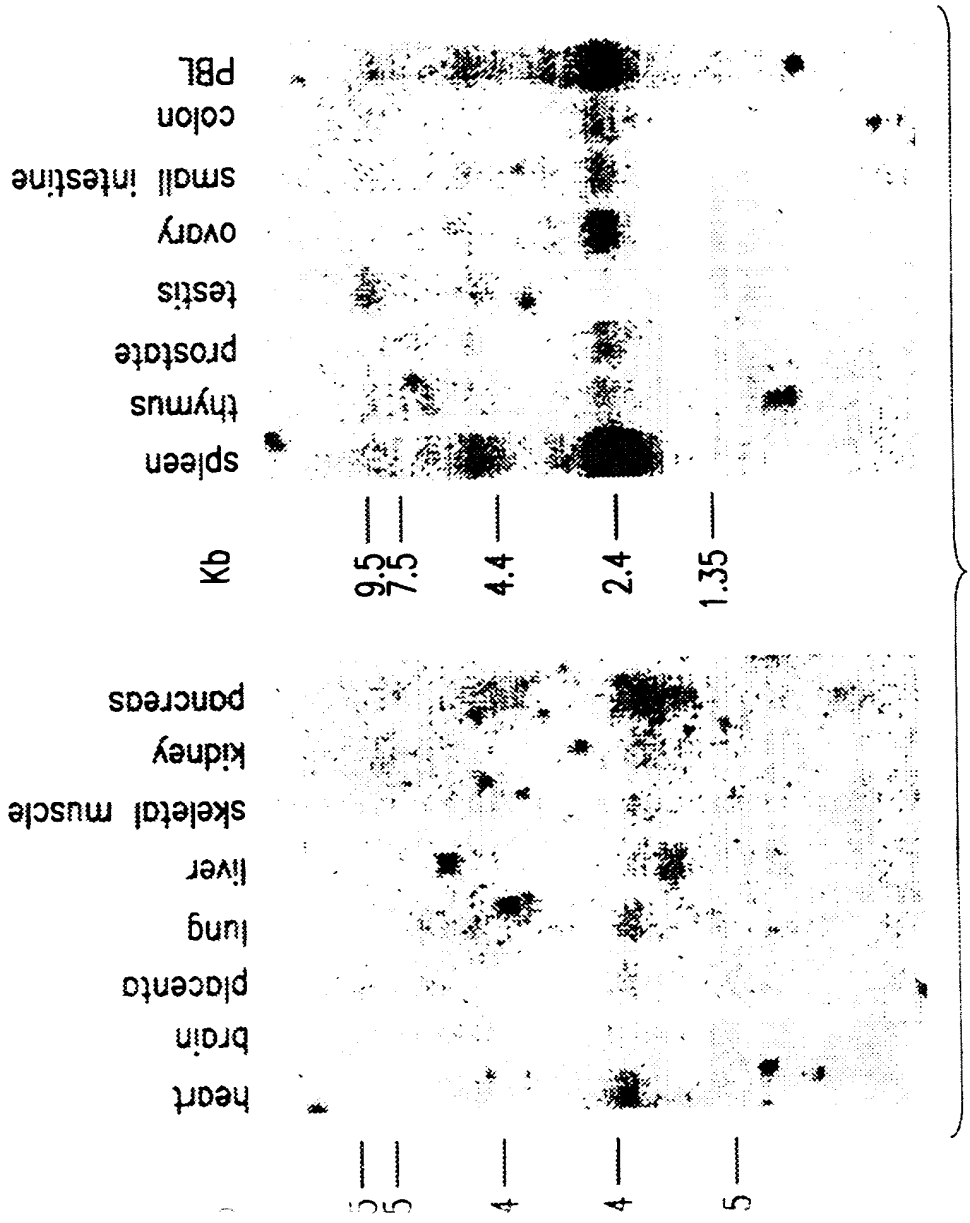
heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas
Kb
9.5
7.5
4.4
2.4
1.35
spleen
thymus
prostate
testis
ovary
small intestine
colon
PBL

FIG.4

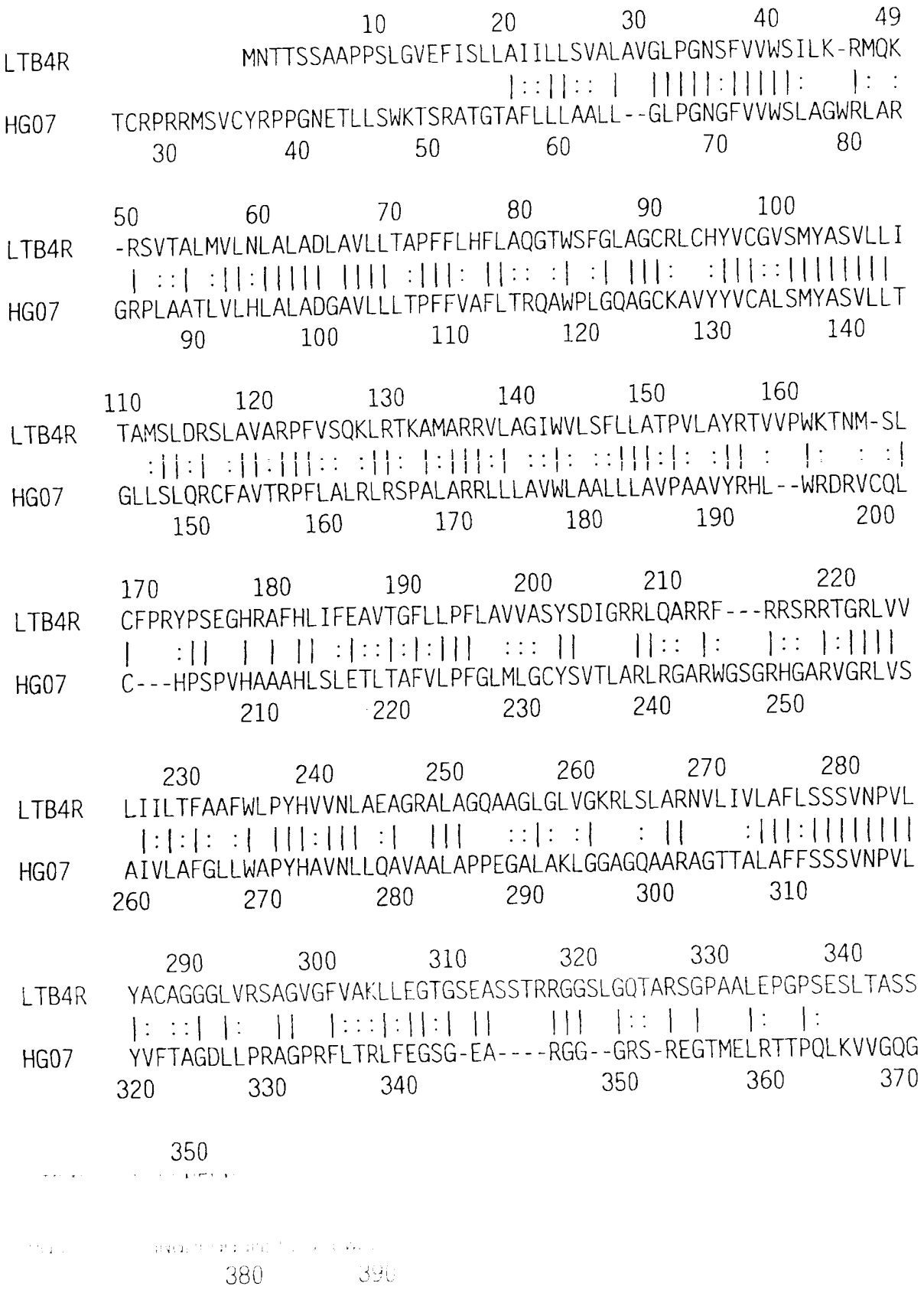
LTB4R MNTTSSAAPPSLGVEFISLLAIILLSVALAVGLPGNSFVVWSILK-RMQK
HG07 TCRPRRMSVCYRPPGNETLLSWKTSRATGTAFLLLAALL--GLPGNGFVVWSLAGWRLAR
LTB4R -RSVTALMVLNLALADLAVLLTAPFFLHFLAQGTWSFGLAGCRLCHYVCGVSMYASVLLI
HG07 GRPLAATLVLHLALADGAVLLLTPFFVAFLTRQAWPLGQAGCKAVYYVCALSMYASVLLT
LTB4R TAMSLDRSLAVARPFVSQKLRTKAMARRVLAGIWVLSFLLATPVLAYRTVVPWKTNM-SL
HG07 GLLSLQRCFAVTRPFLALRLRSPALARRLLLAVWLAALLLAVPAAVYRHL--WRDRVCQL
LTB4R CFPRYPSEGHRAFHLIFEAVTGFLLPFLAVVASYSDIGRRLQARRF---RRSRRTGRLVV
HG07 C---HPSPVHAAAHLSLETLTAFVLPFGLMLGCYSVTLARLRGARWGSGRHGARVGRLVS
LTB4R LIILTFAAFWLPYHVVNLAEAGRALAGQAAGLGLVGKRLSLARNVLIVLAFLSSSVNPVL
HG07 AIVLAFGLLWAPYHAVNLLQAVAALAPPEGALAKLGGAGQAARAGTTALAFFSSSVNPVL
LTB4R YACAGGGLVRSAGVGFVAKLLEGTGSEASSTRRGGSLGQTARSGPAALEPGPSESLTASS
HG07 YVFTAGDLLPRAGPRFLTRLFEGSG-EA----RGG--GRS-REGTMELRTTPQLKVVGQG

FIG.5